

# WEST Search History

DATE: Tuesday, January 07, 2003

## Set Name Query

side by side

## Hit Count Set Name

result set

*DB=USPT,PGPB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=OR*

L8	L7 and (@PD<19961028 or @RLAD<19961028)	10	L8
L7	(2D7 or PA14) and (chemokine or HIV)	105	L7
L6	(HDG NR10 or 88-C) and chemokine	20	L6
L5	L4 and (@PD<19961028 or @RLAD<19961028)	40	L5
L4	L3 and antibody	455	L4
L3	L2 and chemokine	588	L3
L2	(CCR5 or CC-CkR5 or CCCKR5 or CKR5 or ChemR13 or CMKBR5 or CCR-5)	706	L2

*DB=USPT; THES=ASSIGNEE; PLUR=YES; OP=OR*

L1	5939320.pn. or 5994515.pn. or 6025154.pn.	3	L1
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END OF SEARCH HISTORY



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## SEARCH GeneCards


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### RESULT:

5 GeneCards match **your precise query** for "CCR5";

Each is represented by a minicard.

Click "Display" on the left to get the full GeneCard.

**Display**  
the complete  
GeneCard  
for this  
gene  
(CCR5)

**More like this**

**Gene:** CCR5 = chemokine (C-C motif) receptor 5 [Locus: 3p21]

The following lines in the GeneCard text contribute to matching your query:

- GENE: CCR5 (chemokine (C-C motif) receptor 5)
- MOUSE HOMOLOG: Ccr5 (on chromosome 9, 72.00 | Oct 18 2002 | gbaccs: AF019772 AF022990 D83648 U47036 U68565 U83327 X94151 cM)
- SWISSPROT: C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5) (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen)
- SWISSPROT: GENE: CCR5 OR CMKBR5
- HGMD: 1230510 | HGMD entry for CCR5 | mutations
- UNIGENE: Hs.54443 | chemokine (C-C motif) receptor 5 | Build 155: Homo sapiens; Sep 23 2002 | CCR5 | NM\_000579
- LITERATURE: 8663314 | Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha. | SP || 8639485 | Molecular cloning and functional expression of a new human CC-chemokine receptor gene. | HUGO
- GENATLAS: biochem: chemokine CC,beta, receptor 5, expressed in lymphoid organs and cells, with multiple transcripts with 5' end heterogeneity and dual promoter usage, mediating macrophage-tropic strains of HIV-1 entry in CD4+ cells with a reduced risk of AIDS lymphoma in patients with the CCR5-delta 32 mutation, G protein coupled receptor superfamily | disease
- RZPD: id-CCR5

**Display**  
the complete  
GeneCard  
for this  
gene  
(CCL5)

**More like this**

**Gene:** CCL5 = chemokine (C-C motif) ligand 5 [Locus: 17q11.2-q12]

The following lines in the GeneCard text contribute to matching your query:

- SWISSPROT: FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS. BINDS TO CCR1, CCR3, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT RANTES PROTEIN INDUCES A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).



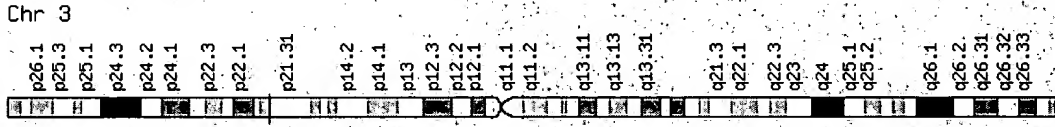
**Display**  
the complete  
GeneCard  
for this  
gene  
(CCL4)

**Gene:** CCL4 = chemokine (C-C motif) ligand 4 [Locus: 17q21-q23]

The following lines in the GeneCard text contribute to matching your query:

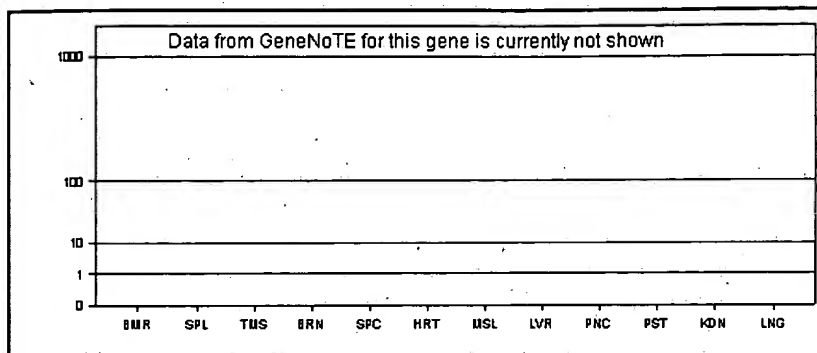
- SWISSPROT: FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES. BINDS TO CCR5 AND TO CCR8. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-BETA INDUCES A

<b>More like this</b>	DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).
<b>Display the complete GeneCard for this gene (CCL3)</b>	<b>Gene:</b> CCL3 = chemokine (C-C motif)-ligand 3 [Locus: 17q11-q21]  <b>The following lines in the GeneCard text contribute to matching your query:</b>  - SWISSPROT: FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES. BINDS TO CCR1, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-ALPHA INDUCES A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).
<b>More like this</b>	
<b>Display the complete GeneCard for this gene (BLR1)</b>	<b>Gene:</b> BLR1 = Burkitt lymphoma receptor 1; GTP binding protein (chemokine (C-X-C motif) receptor 5) [Locus: --]  <b>The following lines in the GeneCard text contribute to matching your query:</b>
<b>More like this</b>	
[ This Search Engine uses <a href="#">glimpse</a> and <a href="#">Excite</a> technology ]	
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Notice - Please read carefully prior to linking to any third-party site							
<b>GeneCard for gene CCR5</b> <b>GC03P045652</b>		Approved <u>UCL/HGNC/HUGO Human Gene Nomenclature database</u> symbol <b>CCR5 (chemokine (C-C motif) receptor 5)</b>					
<b>Aliases and Additional Descriptions</b> (According to <u>GDB</u> , <u>HUGO</u> , and/or <u>SWISS-PROT</u> )		<ul style="list-style-type: none"><li>• CC-CKR-5</li><li>• CCCKR5</li><li>• CKR-5</li><li>• CKR5</li><li>• CMKBR5</li><li>• chemokine (C-C motif) receptor 5</li><li>• C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5) (HIV-1 fus</li></ul>					
<b>Chromosomal Location</b> (According to <u>UDB/GeneLoc</u> and/or <u>HUGO</u> , and/or <u>LocusLink</u> , <u>Genomic Views</u> According to <u>UCSC</u> and <u>Ensembl</u> )		<p><b>Chromosome: 3</b> <u>UDB/GeneLoc gene densities</u></p> <p><b>LocusLink cytogenetic band: 3p21</b> <b>Ensembl cytogenetic band: 3p21.32</b></p> <p><b>Gene in genomic location: bands according to Ensembl, locations according to UDB/GeneL</b></p> <div><p>Chr 3</p></div> <p><b>Unified DataBase (GeneLoc) location for GC03P045652: (about GC identifiers)</b></p> <p><b>Start:</b> 45,652,489 bp from pter</p> <p><b>End:</b> 45,658,542 bp from pter</p> <p><b>Size:</b> 6,053 bases</p> <p><b>Orientation:</b> plus strand</p> <p><b>Unified DataBase (version 2.5) coordinate (from pter): 50.372 mega bases</b></p> <p><b>Genomic View:</b> <u>UCSC Golden Path</u></p>					
<b>Proteins</b> (According to <u>SWISS-PROT</u> and/or <u>MIPS</u> )		<p><b>CKR5 HUMAN</b></p> <ul style="list-style-type: none"><li>• <b>Size:</b> 352 amino acids; 40524 Da</li><li>• <b>Function:</b> RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, M SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULA ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIF WITH CD4 FOR PRIMARY NON- SYNCYTIUM-INDUCING STRAINS (NSI) (MACROI PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.</li><li>• <b>Subcellular location:</b> Integral membrane protein.</li><li>• <b>Tissue specificity:</b> FOUND IN PROMYELOCYTIC CELLS.</li><li>• <b>Ptm:</b> SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.</li><li>• <b>Ptm:</b> MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED GLYCO</li><li>• <b>Similarity:</b> BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.</li></ul> <p><b>MIPS Pedant Viewer:</b> <u>11962</u></p> <p><b>REFSEQ proteins:</b> <u>NP_000570.1</u></p>					
<b>InterPro Domains and Families:</b>							

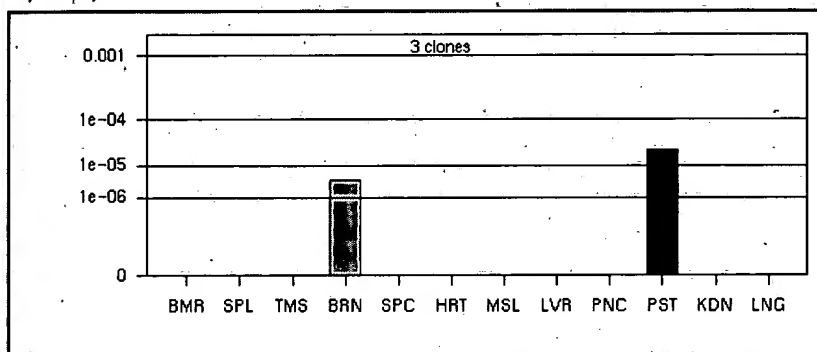
<p><b>Protein Domains/ Families/Ontologies</b> (According to InterPro, GO, and/or BLOCKS)</p>	<p><u>IPR000276; GPCR Rhodpsn</u></p> <p><u>Graphical View of Domain Structure for SP Entry P51681</u></p> <p><b>Gene Ontology (GO) terms (tree view):</b></p> <p><u>GO:0006935</u>  <u>GO:0005887</u>  <u>GO:0007267</u>  <u>GO:0004872</u>  <u>GO:0006954</u>  <u>GO:0016021</u>  <u>GO:0007186</u>  <u>GO:0001584</u>  <u>GO:0007204</u>  <u>GO:0006968</u>  <u>GO:0015026</u>  <u>GO:0007203</u>  <u>GO:0016493</u>  <u>GO:0005768</u>  <u>GO:0007125</u>  <u>GO:0004945</u>  <u>GO:0016494</u></p> <p><b>Blocks protein family:</b> <u>IPB000276 Rhodopsin-like GPCR superfamily</u></p>
<p><b>Sequences</b> (GenBank/EMBL/DDBJ Accessions According to Unigene or GenBank, RefSeq According to LocusLink, Assembly According to MIPS and/or DOTS)</p>	<p><b>REFSEQ mRNAs:</b> <u>NM_000579.1</u></p> <p><b>Additional Gene/cDNA sequence:</b>  <u>AF009962.1 AF011500.1 AF011501.1 AF011502.1 AF011503.1 AF011505.1 AF01150</u>  <u>AF011508.1 AF011509.1 AF011510.1 AF011511.1 AF011512.1 AF011513.1 AF01151</u>  <u>AF011516.1 AF011517.1 AF011518.1 AF011519.1 AF011520.1 AF011521.1 AF01152</u>  <u>AF011524.1 AF011525.1 AF011526.1 AF011527.1 AF011528.1 AF011531.1 AF01153</u>  <u>AF011534.1 AF011535.1 AF011536.1 AF031237.1 BC038398.1 U54994 U54994.1 U5</u>  <u>U57840.1 U83326.1 U95626.1 X91492.1</u></p> <p><b>MIPS assembly:</b> <u>H8606S1</u></p> <p><b>DOTS assembly:</b>  <u>DT.311277</u></p> <p><b>Unigene Cluster for CCR5:</b> ( Build 155 Homo sapiens; Sep 23 2002 )  chemokine (C-C motif) receptor 5  <u>Hs.54443</u> [show with all ESTs]</p> <p><b>Unigene Representative Sequence:</b> <u>NM_000579</u></p> <p><b>CCR5 expression in normal human tissues based on proprietary W.I.S DNA array (Gen</b></p>

**Expression  
in Human Tissues**  
(According to  
proprietary W.I.S DNA  
array results  
(GeneNoTE), UniGene  
and/or SOURCE)



- Immune System
- Nervous System
- Muscle
- Secretory Glands
- Other
- Min-max range for

**CCR5 expression in normal human tissues based on quantifying ESTs from various tissues.**



- Tissue**
- BMR Bone marrow
  - SPL Spleen
  - TMS Thymus
  - BRN Brain
  - SPC Spinal cord
  - HRT Heart
  - MSL Skeletal muscle
  - LVR Liver
  - PNC Pancreas
  - PST Prostate
  - KDN Kidney
  - LNG Lung

SOURCE GeneReport for Unigene cluster Hs.54443

**Similar Genes in  
Other Organisms**  
(According to MGD Oct  
18 2002, Stony Brook  
C.elegans-H.sapiens  
Alignment Database  
and/or euGenes)

**Homologues:**

	gene	locus	description	%similarity to human	G
mouse (MGD)	<u>Ccr5</u>	9 (72.00 cM)	chemokine (C-C motif) receptor 5	--	A U
C. elegans (Stony Brook)	B0454.4	--	Caenorhabditis elegans cosmid B0454, complete sequence	42,61%	A

Variants: SWISS-PROT: CKR5 HUMAN

NCBI SNPs: 10/32 selected, not withdrawn, single nucleotide mutations are shown here.  
Click here to see all of them

**SNPs/Variants**  
(According to the NCBI  
SNP Database and to  
SWISS-PROT)

Genomic Data							
SNP ID	Contig Accession	Pos in Contig	Str	5' Flanking Sequence*	3' Flanking Sequence*	Validation	DNA Chg
rs1799987	NT_034534.1	1955693	+	GAAAAAGGGG	CACAGGGTTA	by-submitter	G/A
rs1799988	NT_034534.1	1956017	+	GTAAATAAAC	TTCAGACCAG	by-submitter	T/C
rs3176763	NT_034534.1	1958034	+	CATCTATGTA	GCAATTAAAA	by-frequency	G/T
rs2856762	NT_034534.1	1957090	+	TATGACCTTC	CTGGGACTTG	by-frequency	C/T
rs3087247	NT_034534.1	1955658	+	GGTTGGGGTG	GATAGGGGAT	by-frequency	C/T
rs3087248	NT_034534.1	1955707	+	AGGGTTAATG	GAAGTCCAGG	by-frequency	G/A
rs3087249	NT_034534.1	1956031	+	AGACCAGAGA	CTATTCTCTA	by-frequency	T/C
rs3087250	NT_034534.1	1956126	+	ACTCCACCCT	CTTCAAAAGA	by-frequency	C/A
rs3181036	NT_034534.1	1956317	+	CCATAGAAGA	ATTTGGCAAA	by-frequency	C/T
rs3181037	NT_034534.1	1956688	+	CAAAATTAAT	TTAAATTACA	by-frequency	A/G

\* Lower case letters indicate repetitive or low-complexity sequence

	All NCBI SNPs in <u>CCR5</u>	
<b>Disorders &amp; Mutations</b> (in which this Gene is Involved, According to <u>OMIM</u> , <u>SWISS-PROT</u> , <u>Genatlas</u> , <u>GeneClinics</u> , <u>HGMD</u> , <u>BCGD</u> , and/or <u>TGDB</u> .)	<b>OMIM ID:</b> 601373  search databases for MIM named disorders: <ul style="list-style-type: none"><li>• <u>{HIV infection, susceptibility/resistance to} (3)</u></li></ul> <b><u>Human Gene Mutation Database</u></b> entry for CCR5	
<b>Medical News</b> (Possibly Related Articles in <u>Doctor's Guide</u> )	<ul style="list-style-type: none"><li>• <u>Gene Protects HIV-Infected People From AIDS But Hastens Death</u></li><li>• <u>Researchers Find Mutation That Slows Down Progression Of HIV</u></li><li>• <u>Mutant Gene Not Sole Explanation for HIV Non-Progression</u></li><li>• <u>A Molecular Mechanism that Allows HIV to Enter Human Cells Identified</u></li><li>• <u>Hidden 'Second Structure' Critical in AIDS Virus Attack</u></li><li>• <u>Scientists Discover Second Gene Alteration That Slows Progression To AIDS</u></li></ul>	
<b>Research Articles</b> (in <u>PubMed</u> )	<ul style="list-style-type: none"><li>• <u>Molecular cloning and functional characterization of a novel human CC chemokine receptor MIP-1alpha.</u></li><li>• <u>Molecular cloning and functional expression of a new human CC-chemokine receptor</u></li></ul> <div>Search PubMed for CCR5</div> to find abstracts of <b>research articles</b> containing th	
<b>CCR5 in Other Genome Wide Resources:</b> (According to <u>GDB</u> , <u>LocusLink</u> , <u>euGenes</u> , <u>Ensembl</u> and/or <u>GeneLynx</u> )	<u>GDB: 1230510</u> <u>LocusLink: 1234</u> <u>euGenes: HUgn1234</u> <u>Ensembl: ENSG00000160</u>	
<b>CCR5 in General Databases, Limited Scope</b> (According to <u>HUGE</u> )		
<b>CCR5 in Specialized Databases</b> (According to <u>ATLAS</u> , <u>GENATLAS</u> , <u>HORDE</u> , <u>IMGT</u> , <u>MTDB</u> , <u>LEIDEN</u> and/or <u>SWISS-PROT</u> )	<i>name</i> <b><u>Genatlas</u></b> biochemistry entry for CCR5: chemokine CC,beta,receptor 5,expressed in lymphoid organs and cells,with multiple transcripts with 5' end heterogeneity and dual promoter usage,mediating macrophage-tropic strains of HIV-1 entry in CD4+ cells with a reduced risk of AIDS lymphoma in patients with the CCR5-delta 32 mutation,G protein coupled receptor superfamily	<i>description</i>  Links to se
<b>Services</b> (According to <u>RZPD</u> )	<u>Search RZPD for clones of CCR5</u> Clone collection at the German Human Genome Project	

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Go

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Display the GeneCard of a random HUGO-approved gene

The GeneCards **idea** in brief: **Mining the Internet** for biomedical knowledge and **guiding** the user to it.

Developed at the Crown Human Genome Center & Weizmann Institute of Science

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